DEVELOPMENT OF END-USER PREFERRED SWEETPOTATO VARIETIES IN GHANA

BY
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Outline of Presentation

- ❑ Background
  1. Materials and Methods
  2. Results
- ❑ Conclusions
- ❑ Acknowledgements

Background

Figure 1. Some innovative sweetpotato products - Source: Adu-Kwarteng et al., 2001.

Background

- Locally available clones have very sweet taste, which limits consumption as a staple food (Missah and Kissiedu, 1994)

- The sweet taste, due to sugars, is the central feature that significantly modulates the overall flavor (Wang and Kays, 2003)

- Recently introduced orange-fleshed varieties have low dry matter content

- Preference for sweetpotato varies with ethnic background and geographic location (Kays and Horvat, 1983)

Background

- ❑ Low adoption of the improved varieties.

Figure 2. Four of the 13 released varieties

Specific objectives

1. Ascertain stakeholders' knowledge, perceptions, and preferences on sweetpotato end-user-traits in Ghana

2. Assess genetic variation of sweetpotato genotypes in Ghana using agro-morphological, physico-chemical and SSR markers

3. Assess self- and cross-compatibility in sweetpotato germplasm

4. Determine the gene action involved in the control of beta-carotene, dry matter and sugar contents of storage roots

5. Determine level of heterosis for beta-carotene, dry matter and sugar contents of sweetpotato storage roots

Objective 1

Ascertain stakeholders' knowledge, perceptions, and preferences on sweetpotato end-user-traits in Ghana

Materials and Methods

Study areas

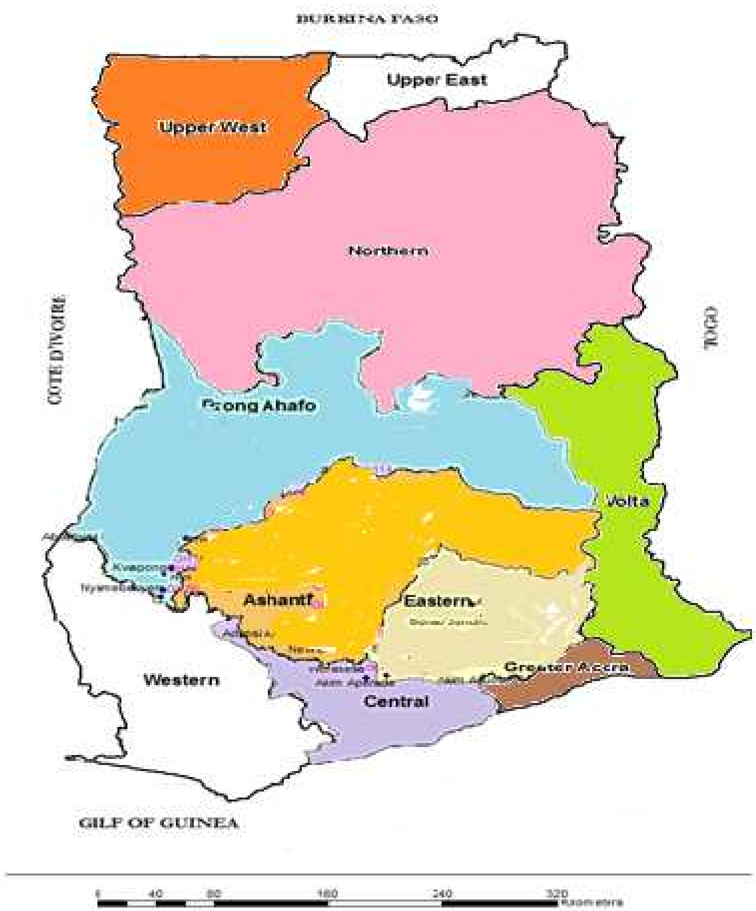

Figure 3. Map of Ghana showing areas PRA was done

- ❑ **2012**
- ❑ **methodology**

1. Focus Group Discussions (FDG)

2. Administration of Semi-structured Questionnaire (SSQ)

❑ **Data analysis**

1. **FGD – GenStat**
2. **SSQ - SPSS**

RESULTS

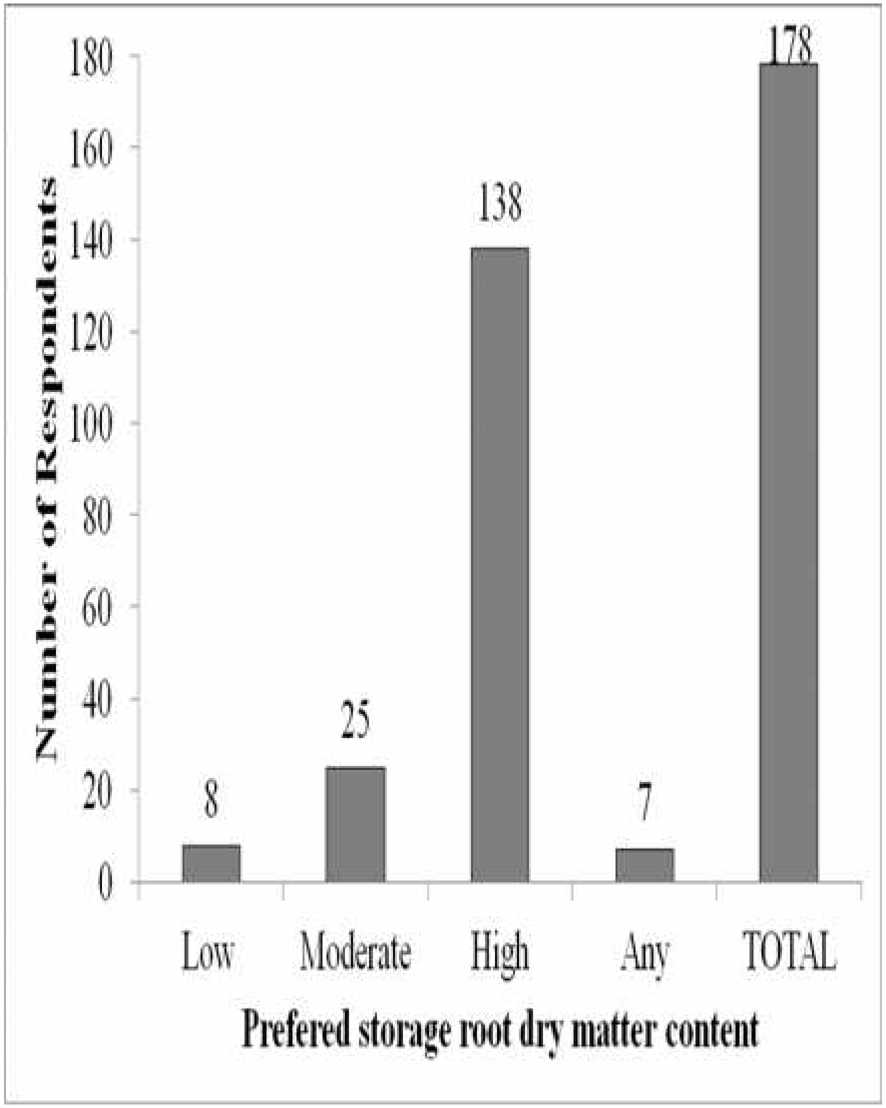

Figure 3. Preferred storage root dry matter content distribution

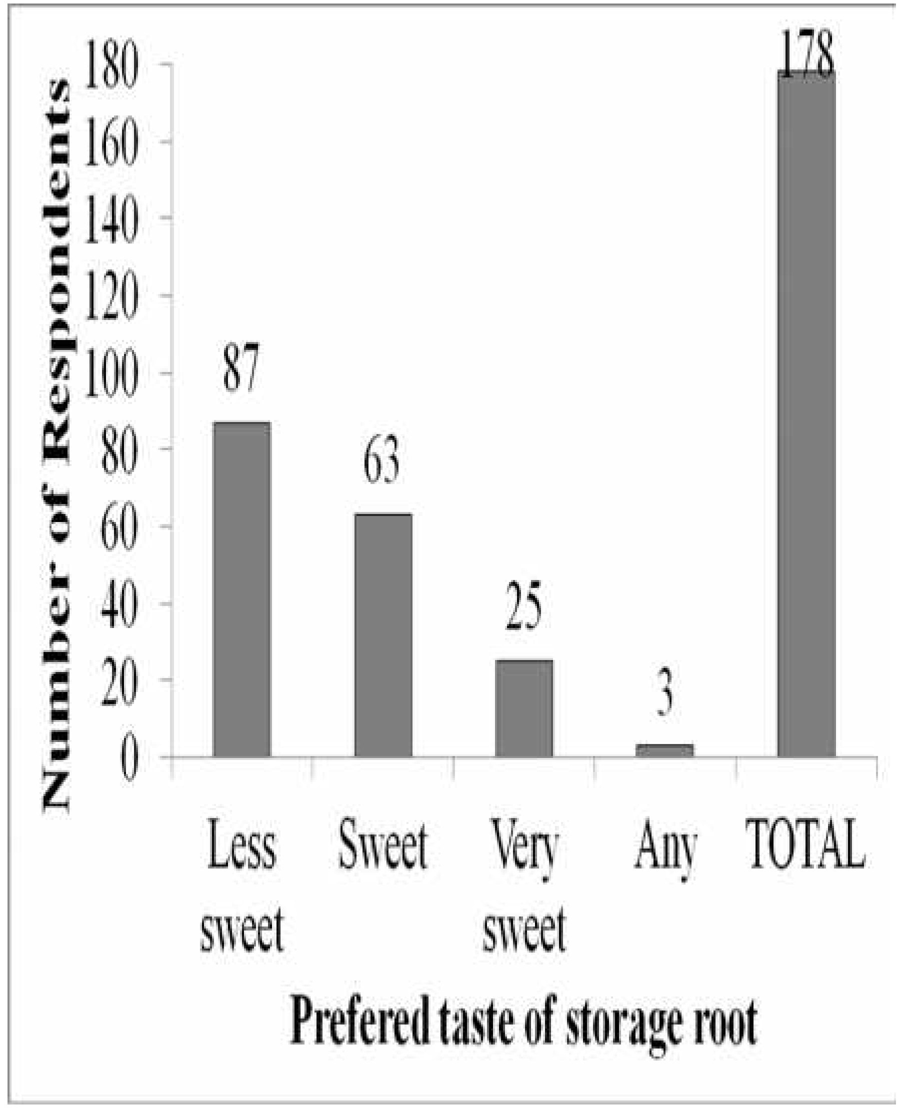

Figure 4. Preferred storage root taste (sweetness) preference

RESULTS

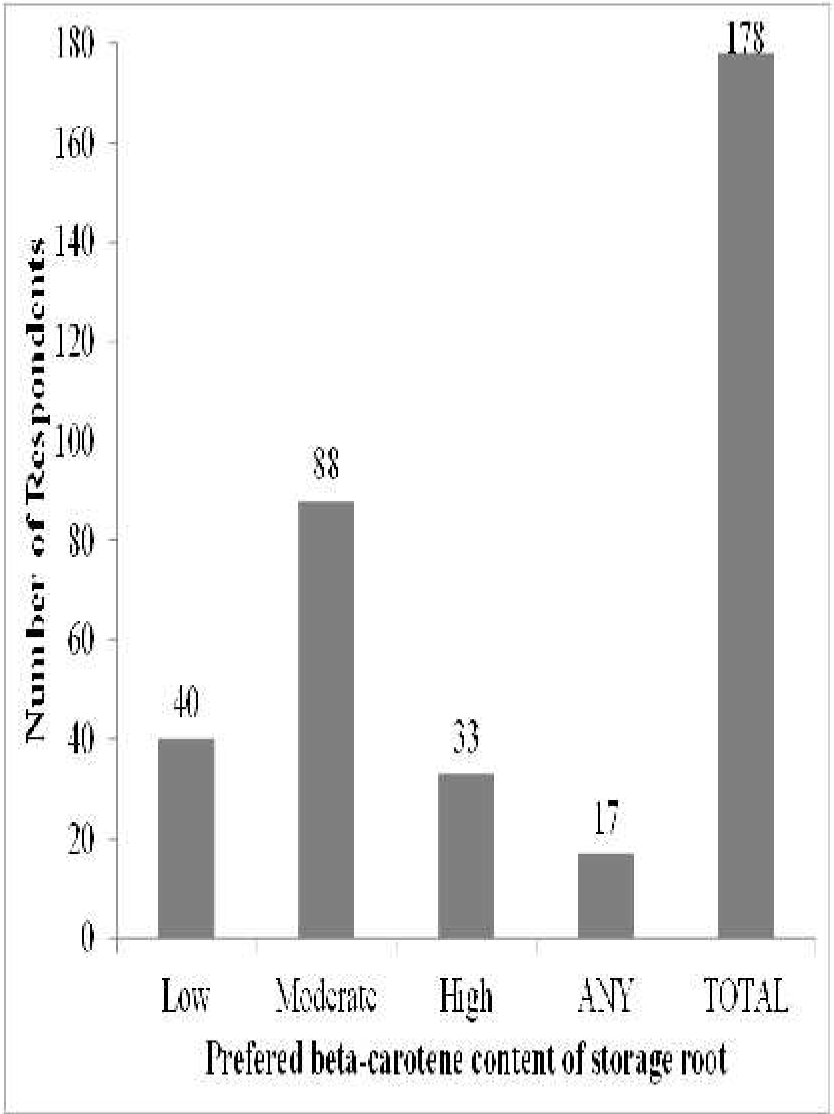

Figure 5. Preferred beta-carotene content of storage root

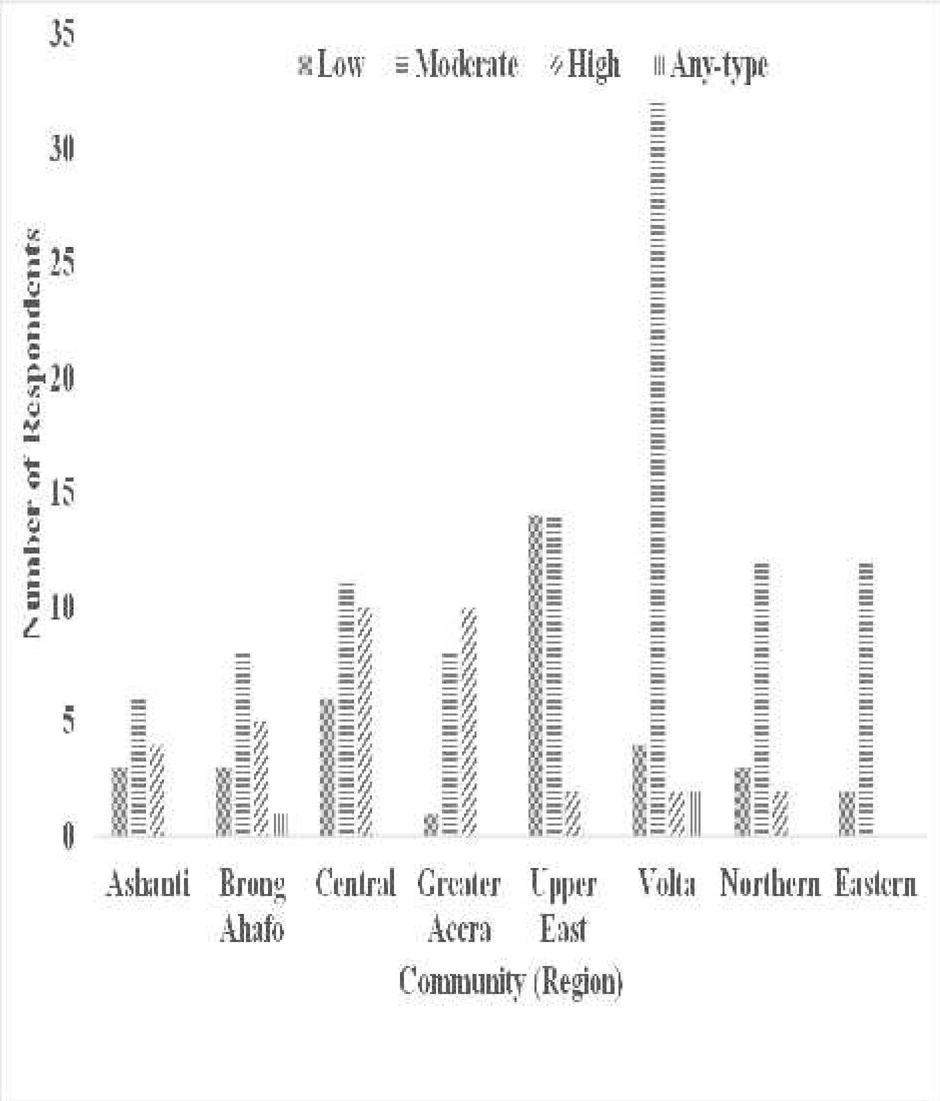

Figure 6. community x beta-carotene preference

Objective 2

Assess genetic variation of sweetpotato genotypes in Ghana and their utilization for breeding

Materials and Methods

1. Phenotypic Characterization

- 115 sweetpotato accessions collected for study
- Location – Fumesua
- Data collection - sweetpotato descriptor for phenotyping (CIP/AVRDC/IBPGR, 1991) & physico-chemical traits

- Data analysis
  - ✓ PCA and Clustering using GenStat version 9.2.0.152 (Genstat, 2007)
  - ✓ GGE biplot (Yan and Kang, 2003)

Materials and Methods

2. Molecular Characterization

- 76 sweetpotato accessions
- 25 SSR markers (Buteler et al. 1999; Diaz and Gruneberg 2008; Tumwegamire et al. 2011)
- Location – CSIR-CRI, Ghana and ICRISAT, India

- Data analysis
  - ✓ NTSYSpc software version 2.1 (Rohlf, 1993; Rohlf, 2002) – for the binary data
  - ✓ Principal coordinate analysis (PCoA) - (Genstat, 2007)
  - ✓ Polymorphic information content (PIC) (Weir,1996)
  - ✓ Analysis of Molecular Variance (Excoffier *et al.*, 2006)

Materials and Methods

3. Estimation of Genetic Parameters

- 115 sweetpotato accessions
- Location –
  - ✓ Field work - Fumesua (Forest ecozone) and Pokuase (Coastal Savannah ecozone) both major and minor seasons in 2011
  - ✓ RCBD in 2 reps was used
  - ✓ Root quality data – NIRS Lab. at CSIR-CRI, Ghana and Lima, Peru
- Data analysis
  - ✓ method of Steel and Torrie (1980)
  - ✓ The variance components determined (Prasad *et al.,* 1981)
  - ✓ h^2_b, GCV, PCV and GA determined (Burton, 1952; Johnson *et al.*, 1955; Kumar *et al.*, 1985)
  - ✓ Genotypic correlation coefficient computed using Miller *et al.* (1958) and (IRRI, 2006)

RESULTS

Table 1 Principal Component Analysis of the agro-morphological and physico-chemical traits

Trait	PC1	PC2	PC3	PC4	PC5	PC6
Root weight	**-0.371**	-0.091	-0.133	0.005	-0.028	-0.033
Marketable root wgt.	**-0.362**	-0.082	-0.139	0.021	-0.003	-0.008
Unmarketable yield.	**-0.370**	-0.094	-0.128	-0.002	-0.038	-0.043
β-carotene	0.168	**-0.310**	-0.128	-0.050	-0.030	0.024
Dry matter	0.168	**0.310**	0.128	0.050	0.030	0.024
Total sugar	0.029	**-0.404**	0.133	0.030	-0.012	-0.025
Sucrose	0.018	-0.235	0.145	0.191	**-0.336**	-0.143
Fructose	0.041	-0.259	-0.056	-0.257	**0.343**	0.173
Glucose	0.023	**-0.316**	0.020	-0.212	**0.307**	0.143
Iron	0.172	-0.035	**-0.416**	0.063	-0.126	-0.099
Zinc	0.157	-0.021	**-0.364**	0.147	-0.249	-0.140
Protein	0.114	0.071	**-0.401**	0.107	-0.178	-0.125
Starch	-0.141	0.144	**0.361**	0.201	-0.133	-0.018
Rt. Oxidation	-0.064	0.020	-0.111	0.069	-0.032	**0.414**

***Values in bold indicate the most relevant characters (>0.3) that contributed most to the variation of the particular component**

RESULTS

Table 2. Analysis of molecular variance (AMOVA) for the 76 sweetpotato accession

Source of variation	Df	Sum of squares	Variance components	Percentage of Variation
Among groups	3	55.894	0.35619*	2.88
Within groups	72	865.198	12.01664**	97.12
Total	75	921.092	12.37284	

*Significant at 0.05 **Significant at 0.01

RESULTS

Table 3. Genotypic correlation coefficient for the physico-chemical and agronomical traits of sweetpotato accessions

Trait	DM	BC	F	G	S	TS	ST	P	Fe	Zn	HI	RWT	MKTRWT
DM		-1.20	**-0.76**	**-0.78**	-0.23	**-0.77**	0.71	0.08	-0.11	0.18	**-0.69**	-0.12	-0.06
BC			0.30	**0.62**	**0.74**	0.56	**-0.61**	0.15	**0.74**	**0.58**	-0.41	-0.41	-0.41
F				**0.98**	0.04	**0.85**	**-0.61**	-0.24	0.02	-0.22	0.30	0.06	0.01
G					0.05	**0.91**	**-0.78**	-0.19	0.11	-0.10	0.30	0.06	0.01
S						**1.09**	**-0.71**	**0.75**	**1.07**	**1.15**	-0.14	-0.42	-0.41
TS							**-0.99**	0.15	**0.60**	0.39	0.22	-0.12	-0.17
ST								0.21	**0.71**	0.39	**0.57**	-0.19	**0.49**
P									**0.75**	**0.75**	0.27	-0.48	-0.46
Fe										**0.90**	-0.08	**-0.54**	**-0.62**
Zn											0.00	**-0.51**	**-0.50**
HI												0.56	**0.57**
RWT													**1.00**

DM: Dry matter, BC: Beta-carotene, F: Fructose, G: Glucose, S: Sucrose, TS: Total sugars, ST: Starch, P: Protein, Fe: Iron, Zn: Zinc, HI: Harvest index, RWT: Root weight, MKTRWT: Marketable root weight

RESULTS

Table 4. Genotypic and phenotypic coefficient of variation, heritability and expected genetic advance for the traits

Trait	Genotypic coefficient of variation	Phenotypic coefficient of variation	Heritability (H^2_b)	Expected Selection Gain (R)	Expected Selection Gain (R %of mean)
Dry matter	7.60	9.61	0.63	0.05	12.37
Beta-carotene	40.28	42.36	0.90	9.03	78.90
Fructose	55.48	60.18	0.85	2.12	105.34
Glucose	36.91	39.88	0.86	2.79	70.35
Sucrose	11.93	21.70	0.30	1.38	13.51
Total sugars	18.01	21.59	0.70	5.10	30.95
Starch	4.07	4.78	0.72	4.89	7.13
Protein	12.46	15.58	0.64	0.91	20.40
Iron	6.80	8.70	0.61	0.22	10.96
Zinc	8.08	9.90	0.65	0.14	13.60
Harvest index	36.80	39.53	0.84	0.27	68.40
Root weight	50.13	55.13	0.83	2.42	93.83
Marketable Root weight	55.35	63.40	0.76	2.01	99.40

Objective 3 - 5

- Combining Ability studies

  1. Compatibility status

  2. Gene action

  3. Population development

Materials and Methods

- ❑ **Beta-carotene/Dry matter – 12 x 12 full diallel**
- ❑ **Sugars – 15 x 15 full diallel**

Table 5. Full diallel representation for the beta-carotene crossing block

Parents	Low beta-carotene							High beta-carotene				
	P1	P2	P3	P4	P5	P6	P7	P8	P9	P10	P11	P12
P1												
P2												
P3												
P4										CROSSES		
P5												
P6												
P7												
P8												
P9												
P10				RECIPROCAL CROSSES				HIGH β-			CAROTENE	
P11												
P12												

Materials and Methods

- ❑High beta-carotene Population
- ❑Low sugar population

Table 6. Genetic materials used for population development

Parents	Dry matter content (%)	Beta-carotene content (mg/100g)DW	Sugar content (%)
Histarch	45	9.85	10.13
Ogyefo	42	6.83	11.67
AAT – 03 – 025	39	10.98	12.26
CIP 442264	45	7.74	11.06
*Resisto	38	27.53	18.53
*Beauregard	32	24.31	22.90
*Apomuden	27	33.67	28.97
*CIP 443035	36	19.75	14.98
*CIP 442850	27	20.21	30.34

* Parents used for the development of high beta-carotene population

Materials and Methods

- **F1 evaluation**

- **LOC –** Fumesua (Forest), Wenchi (Transition), and Pokuase (Coastal Savannah)

- **Data analysis**

- **Gene action**

– Gardner and Eberhart (1966) Analysis II

- **Population development**

- Mid-parent & better parent heterosis determined **(**Fonseca and Patterson,1968; Wynne et al., 1970)

RESULTS

Table 7. Number of crosses conducted to generate F_1 for studies on sugar content of sweetpotato

Parents	S50	S48	S43	S113	S82	S15	S109	S75	S61#	S87#	S97#	S31#	S64#	S72#	S74#
S50	*				102	4	81		112	143	1	53	3	74	
S48		*								4					
S43			*						35	423		6		13	
S113				*					13	4		1		7	
S82	35				*		13		20	42		2			
S15						*			57	145		72		37	
S109	20				6		*		6	22					
S75								*	54	37		38		1	
S61#	29		3		25	27	14	8	*	29					
S87#		6	203	24	142	315	37	31	137	*				12	
S97#											*				
S31#	6			4		5	3	10	3	3		*			
S64#													*		
S72#	19						1	4	1					*	
S74#															*

#Low sugar parent. Light green quadrant = crosses between low and high sugar parent; dark green= reciprocal crosses; Pink=crosses among low sugar clones. S50 (Apomuden), S48 (CIP 440071), S43 (Paga 01), S113 (Ukerewe), S82 (Beauregard), S15 (B/Faso 002), S109 (CIP 442850),), S75 (B/Faso 001), S61 (Ogyefo), S87 (Histarch), S97 (Ebiamankyene 01), S31 (CIP 440095), S64 (CIP 442264), S72 (AAT 03 025), S74 (Ouagadougou 02)

RESULTS

Table 8. Success rate and germination percentage of the crosses

Cross	Number of crosses	Success rate (%)	Seeds per capsule	Percent germination (%)
61 x 87	27	51.9	1.86	95.2
61 x 50	29	51.7	3.53	88.0
61 x 82	25	52.0	1.08	100.0
64 x 87	5	60.0	1.33	100.0
79 x 50	10	50.0	3.00	100.0
79 x 109	1	100.0	3.00	100.0
"	"	"	"	"
"	"	"	"	"
79 x 21	21	52.4	0.18	100.0
79 x 82	2	50.0	4.00	90.9
21 x 50	12	50.0	0.50	100.0
82 x 87	42	50.0	0.71	100.0
82 x 50	35	72.0	1.72	96.9
82 x 109	13	53.9	0.14	100.0
82 x 79	11	54.5	0.67	100.0
Mean	45.41	54.1	1.21	96.3

87=Histarch; 61=Ogyefo; 50=Apomuden; 82=Beauregard;
64=CIP 442264; 79=CIP 443035; 109=CIP 442850; 21=Resisto

RESULTS

Table 9. Genetic material used for the gene action study

Parents	Dry matter content (%)	β-carotene content (mg/100g)DW	Sugar content (%)
Apomuden	27.0	33.67	28.97
Beauregard	32.0	24.31	22.90
Histarch	45.0	9.85	10.43
Ogyefo	42.0	6.83	11.67

RESULTS

Table10. Mean squares (Gardner and Eberhart, 1966 Analysis II) for four parents, their crosses and reciprocals across three environments

Source of variation	Df	β-carotene content	Dry matter content	Sugar content	Starch content	Iron content	Zinc content
CROSSES							
Environment (Env.)	2	23.974^{ns}	0.0005^{ns}	51.77**	37.50*	1.18**	0.73**
Rep. (Env.)	3	4.696^{ns}	0.0002^{ns}	8.20^{ns}	2.19^{ns}	0.05^{ns}	0.02^{ns}
Entry	9	801.825**	0.0193**	294.76**	408.02**	0.64**	0.21**
Env. x Entry	18	13.436^{ns}	0.8000^{ns}	8.61^{ns}	5.81^{ns}	0.05^{ns}	0.02**
Overall heterosis (h_{ij})	5	305.932**	0.0017*	74.38**	107.11**	0.360**	0.1056^{ns}
Average heterosis (h)	1	533.216**	0.0014^{ns}	5.48^{ns}	41.85*	1.141**	0.2310*
Variety heterosis (h_j)	3	264.286**	0.0032**	132.78**	107.70**	0.233^{ns}	0.1992^{ns}
SCA	2	104.175**	0.0014^{ns}	13.453^{ns}	17.40^{ns}	0.001^{ns}	0.0003^{ns}
RECIPROCALS							
Environment (Env.)	2	26.08*	0.0019^{ns}	29.21**	43.69**	1.43**	0.90**
Rep. (Env.)	3	2.87^{ns}	0.0005^{ns}	10.10**	3.37^{ns}	0.03^{ns}	0.02^{ns}
Entry	9	719.56**	0.0214**	288.60**	426.35**	0.72**	0.23**
Env. x Entry	18	11.24*	0.0005^{ns}	6.40**	4.48^{ns}	0.05*	0.02*
Overall heterosis (h_{ij})	5	213.01**	0.0036**	88.99**	158.11**	0.36**	0.129*
Average heterosis (h)	1	686.72**	0.0001^{ns}	37.64**	75.05**	1.03**	0.210*
Variety heterosis (h_j)	3	90.03**	0.0049**	113.12**	206.65**	0.30*	0.145*
SCA	2	80.17**	0.0015^{ns}	34.01**	47.88**	0.02^{ns}	0.003^{ns}

*Significant at P< 0.05; **Significant at P<0.01; ^{ns} Not significant

RESULTS

Table 11. Estimates of mid-parent heterosis (Hb) and heterobeltiosis (Hbt) for the F1 hybrids of Histarch (87) and Ogyefo (61)

Genotype	Dry matter		Total sugars		Starch		Protein		β-carotene		Iron		Zinc		Root yield	
	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)
61x87-11	3^{ns}	-3^{ns}	-39.9*	-33.9*	3.1^{ns}	3.0^{ns}	26.6^{ns}	22.6^{ns}	33.2^{ns}	19.4^{ns}	-10.8^{ns}	-13.1^{ns}	7.9^{ns}	3.3^{ns}	-6.6^{ns}	-22.6^{ns}
87x61-26	-14*	-18*	-39.1*	-33.0*	-3.6^{ns}	-3.7^{ns}	86.4**	80.5**	60.5^{ns}	43.9^{ns}	19.5*	16.5^{ns}	18.7*	13.7^{ns}	-	-
87x61-13	3^{ns}	-2^{ns}	-36.6*	-30.3*	4.6*	4.6*	7.3^{ns}	4.0^{ns}	-46.6^{ns}	-52.1^{ns}	-0.3^{ns}	-2.9^{ns}	0.63^{ns}	-3.6^{ns}	-4.0^{ns}	-20.2^{ns}
87x61-21	1^{ns}	-4^{ns}	-33.6*	-27.0*	0.1^{ns}	0.0^{ns}	41.6*	37.2^{ns}	-36.0^{ns}	-42.6^{ns}	7.6^{ns}	4.8^{ns}	15.3^{ns}	10.4^{ns}	-29.6^{ns}	-41.7^{ns}
87x61-37	-1^{ns}	-6^{ns}	-28.0*	-20.8*	-0.4^{ns}	-0.5^{ns}	3.0^{ns}	-0.2^{ns}	19.8^{ns}	7.4^{ns}	-7.8^{ns}	-10.1^{ns}	7.2^{ns}	2.6^{ns}	64.7^{ns}	36.5^{ns}
87x61-65	2^{ns}	-3^{ns}	-25.4^{ns}	-17.9*	1.7^{ns}	1.7^{ns}	4.5^{ns}	1.2^{ns}	-20.0^{ns}	-28.3^{ns}	-7.6^{ns}	-10.0^{ns}	3.2^{ns}	-1.2^{ns}	-12.9^{ns}	-27.9^{ns}
87x61-87	-4^{ns}	-9^{ns}	-21.8^{ns}	-14.0^{ns}	-1.1^{ns}	-1.2^{ns}	43.3*	38.8^{ns}	52.0^{ns}	36.3^{ns}	8.4^{ns}	5.6^{ns}	14.8^{ns}	9.9^{ns}	-55.9^{ns}	-63.5*
87x61-88	1^{ns}	-4^{ns}	-21.5^{ns}	-13.7^{ns}	1.9^{ns}	1.9^{ns}	6.5^{ns}	3.2^{ns}	-21.7^{ns}	-29.8^{ns}	-9.8^{ns}	-12.1^{ns}	7.45^{ns}	2.9^{ns}	-15.3^{ns}	-29.8^{ns}
"	"	"	"	"	"	"	"	"	"	"	"	"	"	"	"	"
61x87-4	-7^{ns}	-12^{ns}	8.5^{ns}	19.4^{ns}	-0.9^{ns}	-1.0^{ns}	-9.4^{ns}	-12.2^{ns}	-25.4^{ns}	-33.1^{ns}	-6.3^{ns}	-8.7^{ns}	-5.4^{ns}	-9.4^{ns}	30.9^{ns}	8.5^{ns}
87x61-47	-9^{ns}	-14^{ns}	8.7^{ns}	19.6^{ns}	-2.1^{ns}	-2.1^{ns}	-0.1^{ns}	-3.3^{ns}	-7.8^{ns}	-17.3^{ns}	-6.3^{ns}	-8.7^{ns}	2.7^{ns}	-1.6^{ns}	11.7^{ns}	-7.4^{ns}
87x61-46	-8^{ns}	-13^{ns}	14.7^{ns}	26.1^{ns}	-3.5^{ns}	-3.6^{ns}	-16.7^{ns}	-19.3^{ns}	51.3^{ns}	35.7^{ns}	-13.0^{ns}	-15.3^{ns}	-3.1^{ns}	-7.2^{ns}	-79.3*	-82.8*
87x61-57	-9^{ns}	-14^{ns}	17.0^{ns}	28.7^{ns}	-4.2*	-4.3^{ns}	13.7^{ns}	10.1^{ns}	-39.8^{ns}	-46.0^{ns}	-2.5^{ns}	-5.0^{ns}	9.4^{ns}	4.8^{ns}	17.7^{ns}	-2.5^{ns}

*Significant at $P<0.05$; **Significant at $P<0.01$; ^{ns}Not significant at $P<0.05$

RESULTS

Table 12. Performance of Histarch and Ogyefo, and their hybrids

Genotype	Dry matter (%)	Total Sugars (%)	Starch (%)	Protein (%)	β-carotene (mg/100g)DW	Iron (mg/100g)DW	Zinc (mg/100)DW	Root yield (t/ha)
61x87-11	45	9.01	75.14	3.51	5.66	1.36	0.98	16.03
87x61-26	38	9.13	70.22	5.16	6.82	1.82	1.08	-
87x61-13	45	9.50	76.25	2.97	2.27	1.52	0.92	16.53
87x61-21	44	9.94	72.92	3.92	2.72	1.64	1.05	12.08
87x61-37	43	10.79	72.56	2.85	5.09	1.40	0.98	28.26
87x61-65	45	11.18	74.13	2.89	3.40	1.40	0.94	14.94
87x61-87	42	11.72	72.05	3.97	6.46	1.65	1.04	7.57
87x61-88	44	11.76	74.27	2.95	3.33	1.37	0.98	14.54
Ogyefo (61)	41	13.62	72.92	2.86	3.75	1.48	0.95	13.61
87x61-47	40	16.29	71.37	2.77	3.92	1.42	0.93	19.17
Histarch (87)	46	16.33	72.82	2.68	4.74	1.56	0.87	20.71
87x61-46	40	17.18	70.30	2.31	6.43	1.32	0.88	3.56
*SEM (5%)	1.33	1.48	0.97	0.36	1.19	0.09	0.05	4.08
Grand mean	42	13.41	72.77	2.99	4.08	1.44	0.95	16.30
Range	36 – 48	9.01 - 17.53	68.34 - 76.25	1.99 - 5.16	1.63 - 8.23	1.21 - 1.82	0.83 - 1.17	7.57 - 36.31
CV (%)	6.8	20.4	2.5	21.6	54.0	12.3	9.9	46.4

*SEM =Standard error of mean

Conclusions

- Consumers in Ghana desire non-sweet, high dry matter sweetpotatoes with low or moderate beta-carotene content
- Genetic variability was significant for the traits studied and much of this genetic variation was additive in nature
- Significant negative heterosis for sugar content is very important in breeding for non-sweetness
- Non-sweet, high dry matter hybrids were identified
- Adding high beta-carotene content to these types may require many cycles of selection
- Lack or poor flowering was a problem

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